



SEQUENCE LISTING

<110> Vale, Ronald

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<120> Assays for the Detection of Microtubule Depolymerization Inhibitors

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<160> 16

<170> PatentIn version 3.0

<210> 1

<211> 517

<212> PRT

<213> Strongylocentrotus purpuratus

<220>

<221> misc_feature

<223> katanin p60 subunit

<400> 1

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Ala Leu Leu Gly Asn Tyr Glu Thr Ser Leu Val Tyr Tyr Gln Gly Val
20 25 30

Leu Gln Gln Ile Gln Lys Leu Leu Thr Ser Val His Glu Pro Gln Arg
35 40 45

Lys His Gln Trp Gln Thr Ile Arg Gln Glu Leu Ser Gln Glu Tyr Glu
50 55 60

His Val Lys Asn Ile Thr Lys Thr Leu Asn Gly Phe Lys Ser Glu Pro
65 70 75 80

Ala Ala Pro Glu Pro Ala Pro Asn His Gly Arg Ala Ala Pro Phe Ser
85 90 95

His	His	Gln	His	Ala	Ala	Lys	Pro	Ala	Ala	Ala	Glu	Pro	Ala	Arg	Asp	
			100					105					110			
Pro	Asp	Val	Trp	Pro	Pro	Pro	Thr	Pro	Val	Asp	His	Arg	Pro	Ser	Pro	
		115					120					125				
Pro	Tyr	Gln	Arg	Ala	Ala	Arg	Lys	Asp	Pro	Pro	Arg	Arg	Ser	Glu	Pro	
	130					135					140					
Ser	Lys	Pro	Ala	Asn	Arg	Ala	Pro	Gly	Asn	Asp	Arg	Gly	Gly	Arg	Gly	
145					150					155					160	
Pro	Ser	Asp	Arg	Arg	Gly	Asp	Ala	Arg	Ser	Gly	Gly	Gly	Gly	Arg	Gly	
				165					170					175		
Gly	Ala	Arg	Gly	Ser	Asp	Lys	Asp	Lys	Asn	Arg	Gly	Gly	Lys	Ser	Asp	
			180					185					190			
Lys	Asp	Lys	Lys	Ala	Pro	Ser	Gly	Glu	Glu	Gly	Asp	Glu	Lys	Lys	Phe	
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Asp	Pro	Ala	Gly	Tyr	Asp	Lys	Asp	Leu	Val	Glu	Asn	Leu	Glu	Arg	Asp	
	210					215					220					
Ile	Val	Gln	Arg	Asn	Pro	Asn	Val	His	Trp	Ala	Asp	Ile	Ala	Gly	Leu	
225					230					235					240	
Thr	Glu	Ala	Lys	Arg	Leu	Leu	Glu	Glu	Ala	Val	Val	Leu	Pro	Leu	Trp	
				245					250					255		
Met	Pro	Asp	Tyr	Phe	Lys	Gly	Ile	Arg	Arg	Pro	Trp	Lys	Gly	Val	Leu	
			260					265					270			
Met	Val	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Met	Leu	Ala	Lys	Ala	Val	
		275					280					285				
Ala	Thr	Glu	Cys	Gly	Thr	Thr	Phe	Phe	Asn	Val	Ser	Ser	Ala	Ser	Leu	
	290					295					300					
Thr	Ser	Lys	Tyr	His	Gly	Glu	Ser	Glu	Lys	Leu	Val	Arg	Leu	Leu	Phe	
305					310					315					320	
Glu	Met	Ala	Arg	Phe	Tyr	Ala	Pro	Ser	Thr	Ile	Phe	Ile	Asp	Glu	Ile	
				325					330					335		
Asp	Ser	Ile	Cys	Ser	Lys	Arg	Gly	Thr	Gly	Ser	Glu	His	Glu	Ala	Ser	
			340					345					350			
Arg	Arg	Val	Lys	Ser	Glu	Leu	Leu	Ile	Gln	Met	Asp	Gly	Val	Ser	Gly	
		355					360					365				
Pro	Ser	Ala	Gly	Glu	Glu	Ser	Ser	Lys	Met	Val	Met	Val	Leu	Ala	Ala	
						375					380					
Thr	Asn	Phe	Pro	Trp	Asp	Ile	Asp	Glu	Ala	Leu	Arg	Arg	Arg	Leu	Glu	
385					390					395					400	
Lys	Arg	Ile	Tyr	Ile	Pro	Leu	Pro	Glu	Ile	Asp	Gly	Arg	Glu	Gln	Leu	
				405					410					415		
Leu	Arg	Ile	Asn	Leu	Lys	Glu	Val	Pro	Leu	Ala	Asp	Asp	Ile	Asp	Leu	
			420					425					430			

Lys Ser Ile Ala Glu Lys Met Asp Gly Tyr Ser Gly Ala Asp Ile Thr
 435 440 445
 Asn Val Cys Arg Asp Ala Ser Met Met Ala Met Arg Arg Arg Ile Gln
 450 455 460
 Gly Leu Arg Pro Glu Glu Ile Arg His Ile Pro Lys Glu Glu Leu Asn
 465 470 475 480
 Gln Pro Ser Thr Pro Ala Asp Phe Leu Leu Ala Leu Gln Lys Val Ser
 485 490 495
 Lys Ser Val Gly Lys Glu Asp Leu Val Lys Tyr Met Ala Trp Met Glu
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 Glu Phe Gly Ser Val
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 <213> Strongylocentrotus purpuratus
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 <223> katanin p80 subunit
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 Val Thr Gly Gly Glu Asp Lys Lys Val Asn Leu Trp Ala Val Gly Lys
 35 40 45
 Gln Asn Cys Ile Ile Ser Leu Ser Gly His Thr Ser Pro Val Asp Ser
 50 55 60
 Val Lys Phe Asn Ser Ser Glu Glu Leu Val Val Ala Gly Ser Gln Ser
 65 70 75 80
 Gly Thr Met Lys Ile Tyr Asp Leu Glu Pro Ala Lys Ile Val Arg Thr
 85 90 95
 Leu Thr Gly His Arg Asn Ser Ile Arg Cys Met Asp Phe His Pro Phe
 100 105 110
 Gly Glu Phe Val Ala Ser Gly Ser Thr Asp Thr Asn Val Lys Leu Trp
 115 120 125

Asp	Val	Arg	Arg	Lys	Gly	Cys	Ile	Tyr	Thr	Tyr	Lys	Gly	His	Ser	Asp
130						135					140				
Gln	Val	Asn	Met	Ile	Lys	Phe	Ser	Pro	Asp	Gly	Lys	Trp	Leu	Val	Thr
145					150					155					160
Ala	Ser	Glu	Asp	Thr	Thr	Ile	Lys	Leu	Trp	Asp	Leu	Thr	Met	Gly	Lys
				165					170					175	
Leu	Phe	Gln	Glu	Phe	Lys	Asn	His	Thr	Gly	Gly	Val	Thr	Gly	Ile	Glu
			180					185					190		
Phe	His	Pro	Asn	Glu	Phe	Leu	Leu	Ala	Ser	Gly	Ser	Ser	Asp	Arg	Thr
		195					200					205			
Val	Gln	Phe	Trp	Asp	Leu	Glu	Thr	Phe	Gln	Leu	Val	Ser	Ser	Thr	Ser
	210					215					220				
Pro	Gly	Ala	Ser	Ala	Val	Arg	Ser	Ile	Ser	Phe	His	Pro	Asp	Gly	Ser
225					230					235					240
Tyr	Leu	Phe	Cys	Ser	Ser	Gln	Asp	Met	Leu	His	Ala	Phe	Gly	Trp	Glu
				245					250					255	
Pro	Ile	Arg	Cys	Phe	Asp	Thr	Phe	Ser	Val	Phe	Trp	Gly	Lys	Val	Ala
			260					265					270		
Asp	Thr	Val	Ile	Ala	Ser	Thr	Gln	Leu	Ile	Gly	Ala	Ser	Phe	Asn	Ala
		275					280					285			
Thr	Asn	Val	Ser	Val	Tyr	Val	Ala	Asp	Leu	Ser	Arg	Met	Ser	Thr	Thr
	290					295					300				
Gly	Ile	Ala	Gln	Glu	Pro	Gln	Ser	Gln	Pro	Ser	Lys	Thr	Pro	Ser	Gly
305					310					315					320
Gly	Ala	Glu	Glu	Val	Pro	Ser	Lys	Pro	Leu	Thr	Ala	Ser	Gly	Arg	Lys
				325					330					335	
Asn	Phe	Val	Arg	Glu	Arg	Pro	His	Thr	Thr	Ser	Ser	Lys	Gln	Arg	Gln
			340					345					350		
Pro	Asp	Val	Lys	Ser	Glu	Pro	Glu	Arg	Gln	Ser	Pro	Thr	Gln	Asp	Glu
		355					360					365			
Gly	Val	Lys	Asp	Asp	Asp	Ala	Thr	Asp	Ile	Lys	Asp	Pro	Asp	Ser	Tyr
	370					375					380				
Ala	Lys	Ile	Phe	Ser	Pro	Lys	Thr	Arg	Val	Asp	His	Ser	Pro	Glu	Arg
385					390					395					400
Asn	Ala	Gln	Pro	Phe	Pro	Ala	Pro	Leu	Asp	Val	Pro	Gly	Ala	Gln	Glu
				405					410					415	
Pro	Glu	Pro	Phe	Lys	His	Pro	Pro	Lys	Pro	Ala	Ala	Ala	Ala	Ala	Val
			420					425					430		
Ala	Pro	Val	Ser	Arg	Ala	Pro	Ala	Pro	Ser	Ala	Ser	Asp	Trp	Gln	Pro
		435					440					445			

Ala Gln Ala Asn Pro Ala Pro Asn Arg Val Pro Ala Ala Thr Lys Pro
 450 455 460
 Val Pro Ala Gln Glu Val Ala Pro Ser Arg Lys Pro Asp Pro Ile Ser
 465 470 475 480
 Thr Ile Ile Pro Ser Asp Arg Asn Lys Pro Ala Asn Leu Asp Met Asp
 485 490 495
 Ala Phe Leu Pro Pro Ala His Ala Gln Gln Ala Pro Arg Val Asn Ala
 500 505 510
 Pro Ala Ser Arg Lys Gln Ser Asp Ser Glu Arg Ile Glu Gly Leu Arg
 515 520 525
 Lys Gly His Asp Ser Met Cys Gln Val Leu Ser Ser Arg His Arg Asn
 530 535 540
 Leu Asp Val Val Arg Ala Ile Trp Thr Ala Gly Asp Ala Lys Thr Ser
 545 550 555 560
 Val Glu Ser Val Val Asn Met Lys Asp Gln Ala Ile Leu Val Asp Ile
 565 570 575
 Leu Asn Ile Met Leu Leu Lys Lys Ser Leu Trp Asn Leu Asp Met Cys
 580 585 590
 Val Val Val Leu Pro Arg Leu Lys Glu Leu Leu Ser Ser Lys Tyr Glu
 595 600 605
 Asn Tyr Val His Thr Ser Cys Ala Cys Leu Lys Leu Ile Leu Lys Asn
 610 615 620
 Phe Thr Ser Leu Phe Asn Gln Asn Ile Lys Cys Pro Pro Ser Gly Ile
 625 630 635 640
 Asp Ile Thr Arg Glu Glu Arg Tyr Asn Lys Cys Ser Lys Cys Tyr Ser
 645 650 655
 Tyr Leu Ile Ala Thr Arg Gly Tyr Val Glu Glu Lys Gln His Val Ser
 660 665 670
 Gly Lys Leu Gly Ser Ser Phe Arg Glu Leu His Leu Leu Leu Asp Gln
 675 680 685
 Leu Glu
 690

<210> 3

<211> 730

<212> PRT

<213> *Xenopus laevis*

<220>

<221> misc_feature

<223> *Xenopus* kinesin central motor 1 (XKCM1)

<400> 3

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Ile	Met	Arg	Ser	Asn	Gly	Val	Ile	His	Asn	Ala	Asn	Ile	Thr	Ser	Val
			20					25					30		
Asn	Met	Asp	Arg	Ser	Ser	Val	Asn	Val	Glu	Trp	Lys	Glu	Gly	Glu	Ala
		35					40					45			
Asn	Lys	Gly	Lys	Glu	Ile	Ser	Phe	Ala	Asp	Val	Ile	Ser	Val	Asn	Pro
	50					55					60				
Glu	Leu	Leu	Asp	Ala	Val	Leu	Ala	Pro	Thr	Asn	Val	Lys	Glu	Asn	Met
65					70					75					80
Pro	Pro	Gln	Arg	Asn	Val	Ser	Ser	Gln	Asn	His	Lys	Arg	Lys	Thr	Ile
				85					90					95	
Ser	Lys	Ile	Pro	Ala	Pro	Lys	Glu	Val	Ala	Ala	Lys	Asn	Ser	Leu	Leu
			100					105					110		
Ser	Glu	Ser	Gly	Ala	Gln	Ser	Val	Leu	Arg	Glu	Arg	Ser	Thr	Arg	Met
		115					120					125			
Thr	Ala	Ile	His	Glu	Thr	Leu	Pro	Tyr	Glu	Asn	Glu	Met	Glu	Ala	Glu
	130					135					140				
Ser	Thr	Pro	Leu	Pro	Ile	Gln	Gln	Asn	Ser	Val	Gln	Ala	Arg	Ser	Arg
145					150					155					160
Ser	Thr	Lys	Val	Ser	Ile	Ala	Glu	Glu	Pro	Arg	Leu	Gln	Thr	Arg	Ile
				165					170					175	
Ser	Glu	Ile	Val	Glu	Glu	Ser	Leu	Pro	Ser	Gly	Arg	Asn	Asn	Gln	Gly
			180					185					190		
Arg	Arg	Lys	Ser	Asn	Ile	Val	Lys	Glu	Met	Glu	Lys	Met	Lys	Asn	Lys
		195					200					205			
Arg	Glu	Glu	Gln	Arg	Ala	Gln	Asn	Tyr	Glu	Arg	Arg	Met	Lys	Arg	Ala
	210					215					220				
Gln	Asp	Tyr	Asp	Thr	Ser	Val	Pro	Asn	Trp	Glu	Phe	Gly	Lys	Met	Ile
225					230					235					240
Lys	Glu	Phe	Arg	Ala	Thr	Met	Asp	Cys	His	Arg	Ile	Ser	Met	Ala	Asp
				245					250					255	
Pro	Ala	Glu	Glu	His	Arg	Ile	Cys	Val	Cys	Val	Arg	Lys	Arg	Pro	Leu
			260					265					270		
Asn	Lys	Gln	Glu	Leu	Ser	Lys	Lys	Glu	Ile	Asp	Ile	Ile	Ser	Val	Pro
		275					280					285			
Ser	Lys	Asn	Ile	Val	Leu	Val	His	Glu	Pro	Lys	Leu	Lys	Val	Asp	Leu
	290					295					300				
Thr	Lys	Tyr	Leu	Glu	Asn	Gln	Ala	Phe	Arg	Phe	Asp	Phe	Ser	Phe	Asp
305					310					315					320

Glu Thr Ala Thr Asn Glu Val Val Tyr Arg Phe Thr Ala Arg Pro Leu
 325 330 335
 Val Gln Ser Ile Phe Glu Gly Gly Lys Ala Thr Cys Phe Ala Tyr Gly
 340 345 350
 Gln Thr Gly Ser Gly Lys Thr His Thr Met Gly Gly Asp Phe Ser Gly
 355 360 365
 Lys Ser Gln Asn Val Ser Lys Gly Val Tyr Ala Phe Ala Ser Arg Asp
 370 375 380
 Val Phe Leu Leu Leu Asp Gln Pro Arg Tyr Lys His Leu Asp Leu Asp
 385 390 395 400
 Val Phe Val Thr Phe Phe Glu Ile Tyr Asn Gly Lys Val Phe Asp Leu
 405 410 415
 Leu Asn Lys Lys Thr Lys Leu Arg Val Leu Glu Asp Ala Lys Gln Glu
 420 425 430
 Val Gln Val Val Gly Leu Leu Glu Lys Gln Val Ile Ser Ala Asp Asp
 435 440 445
 Val Phe Lys Met Ile Glu Ile Gly Ser Ala Cys Arg Thr Ser Gly Gln
 450 455 460
 Thr Phe Ala Asn Thr Ser Ser Ser Arg Ser His Ala Cys Leu Gln Ile
 465 470 475 480
 Ile Leu Arg Arg Gly Ser Lys Leu His Gly Lys Phe Ser Leu Val Asp
 485 490 495
 Leu Ala Gly Asn Glu Arg Gly Val Asp Thr Ala Ser Ala Asp Arg Ile
 500 505 510
 Thr Arg Met Lys Gly Ala Glu Ile Asn Arg Ser Leu Leu Ala Leu Lys
 515 520 525
 Glu Cys Ile Arg Ala Leu Gly Gln Asn Lys Ser His Thr Pro Phe Arg
 530 535 540
 Glu Ser Lys Leu Thr Gln Ile Leu Arg Asp Ser Phe Ile Gly Glu Asn
 545 550 555 560
 Ser Arg Thr Cys Met Ile Ala Met Leu Ser Pro Gly Phe Asn Ser Cys
 565 570 575
 Glu Tyr Thr Leu Asn Thr Leu Arg Tyr Ala Asp Arg Val Lys Glu Leu
 580 585 590
 Ser Pro Gln Asn Ala Glu Thr Asn Asp Asp Asn Leu Gln Met Glu Asp
 595 600 605
 Ser Gly Gly Ser His Ala Ser Ile Glu Gly Leu Gln Leu Gln Asp Asp
 610 615 620
 Phe Leu Leu Lys Asp Glu Glu Leu Ser Thr His Asn Ser Phe Gln Asp
 625 630 635 640
 Ala Leu Asn Arg Val Gly Glu Leu Glu Asp Lys Ala Val Asp Glu Leu
 645 650 655

Arg Glu Leu Val Gln Lys Glu Pro Glu Trp Thr Asn Leu Leu Gln Met
660 665 670

Thr Glu Gln Pro Asp Tyr Asp Leu Glu Asn Phe Val Met Gln Ala Glu
675 680 685

Tyr Leu Ile Gln Glu Arg Ser Lys Val Leu Ile Ala Leu Gly Asp Ser
690 695 700

Ile Asn Ser Leu Arg Leu Ala Leu Gln Val Glu Glu Gln Ala Ser Lys
705 710 715 720

Gln Ile Ser Lys Lys Lys Arg Ser Asn Lys
725 730

<210> 4

<211> 217

<212> PRT

<213> Strongylocentrotus purpuratus

<220>

<221> misc_feature

<223> AAA ATPase superfamily katanin p60 AAA domain

<400> 4

Val His Trp Ala Asp Ile Ala Gly Leu Thr Glu Ala Lys Arg Leu Leu
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Glu Glu Ala Val Val Leu Pro Leu Trp Met Pro Asp Tyr Phe Lys Gly
20 25 30

Ile Phe Phe Pro Trp Lys Gly Val Leu Met Val Gly Pro Pro Gly Thr
35 40 45

Gly Lys Thr Met Leu Ala Lys Ala Val Ala Thr Glu Cys Gly Thr Thr
50 55 60

Phe Phe Asn Val Ser Ser Ala Ser Leu Thr Ser Lys Tyr His Gly Glu
65 70 75 80

Ser Glu Lys Leu Val Arg Leu Leu Phe Glu Met Ala Arg Phe Tyr Ala
85 90 95

Pro Ser Thr Ile Phe Ile Asp Glu Ile Asp Ser Ile Cys Ser Lys Arg
100 105 110

Gly Thr Gly Ser Glu His Glu Ala Ser Arg Arg Val Lys Ser Glu Leu
115 120 125

Leu Ile Gln Met Asp Gly Val Ser Gly Pro Ser Ala Gly Glu Glu Ser
130 135 140

Ser Lys Met Val Met Val Leu Ala Ala Thr Asn Phe Pro Trp Asp Ile
145 150 155 160

Asp Glu Ala Leu Arg Arg Arg Leu Glu Lys Arg Ile Tyr Ile Pro Leu
 165 170 175
 Pro Glu Ile Asp Gly Arg Glu Gln Leu Leu Arg Ile Asn Leu Lys Glu
 180 185 190
 Val Pro Leu Ala Asp Asp Ile Asp Leu Lys Ser Ile Ala Glu Lys Met
 195 200 205
 Asp Gly Tyr Ser Gly Ala Asp Ile Thr
 210 215
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 <211> 213
 <212> PRT
 <213> Caenorhabditis elegans
 <220>
 <221> misc_feature
 <223> AAA ATPase superfamily mei-1 AAA domain
 <400> 5
 Met Ser Leu Asp Asp Ile Ile Gly Met His Asp Val Lys Gln Val Leu
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 His Glu Ala Val Thr Leu Pro Leu Leu Val Pro Glu Phe Phe Gln Gly
 20 25 30
 Leu Arg Ser Pro Trp Lys Ala Met Val Leu Ala Gly Pro Pro Gly Thr
 35 40 45
 Gly Lys Thr Leu Ile Ala Arg Ala Ile Ala Ser Glu Ser Ser Ser Thr
 50 55 60
 Phe Phe Thr Val Ser Ser Thr Asp Leu Ser Ser Lys Trp Arg Gly Asp
 65 70 75 80
 Ser Glu Lys Ile Val Arg Leu Leu Phe Glu Leu Ala Arg Phe Tyr Ala
 85 90 95
 Pro Ser Ile Ile Phe Ile Asp Glu Ile Asp Thr Leu Gly Gly Gln Arg
 100 105 110
 Gly Asn Ser Gly Glu His Glu Ala Ser Arg Arg Val Lys Ser Glu Phe
 115 120 125
 Leu Val Gln Met Asp Gly Ser Gln Asn Lys Phe Asp Ser Arg Arg Val
 130 135 140
 Phe Val Leu Ala Ala Thr Asn Ile Pro Trp Glu Leu Asp Glu Ala Leu
 145 150 155 160

Arg Arg Arg Phe Glu Lys Arg Ile Phe Ile Pro Leu Pro Asp Ile Asp
 165 170 175
 Ala Arg Lys Lys Leu Ile Glu Lys Ser Met Glu Gly Thr Pro Lys Ser
 180 185 190
 Asp Glu Ile Asn Tyr Asp Asp Leu Ala Ala Arg Thr Glu Gly Phe Ser
 195 200 205
 Gly Ala Asp Val Val
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 <211> 215
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <220>
 <221> misc_feature
 <223> AAA ATPase superfamily sug1 AAA domain
 <400> 6
 Ser Thr Tyr Asp Met Val Gly Gly Leu Thr Lys Gln Ile Lys Glu Ile
 1 5 10 15
 Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu Ser
 20 25 30
 Leu Gly Ile Ala Gln Pro Lys Gly Val Ile Leu Tyr Gly Pro Pro Gly
 35 40 45
 Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys
 50 55 60
 Lys Phe Ile Arg Val Ser Gly Ala Glu Leu Val Gln Lys Tyr Ile Gly
 65 70 75 80
 Glu Gly Ser Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His
 85 90 95
 Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Thr
 100 105 110
 Arg Val Glu Gly Ser Gly Gly Gly Asp Ser Glu Val Gln Arg Thr Met
 115 120 125
 Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Thr Ser Lys Asn Ile
 130 135 140
 Lys Ile Ile Met Ala Thr Asn Arg Leu Asp Ile Leu Asp Pro Ala Leu
 145 150 155 160

Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro Ser
 165 170 175
 Val Ala Ala Arg Ala Glu Ile Leu Arg Ile His Ser Arg Lys Met Asn
 180 185 190
 Leu Thr Arg Gly Ile Asn Leu Arg Lys Val Ala Glu Lys Met Asn Gly
 195 200 205
 Cys Ser Gly Ala Asp Val Lys
 210 215
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 <213> Escherichia coli
 <220>
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 <223> AAA ATPase superfamily ftsH AAA domain
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 Ala Glu Leu Val Glu Tyr Leu Arg Glu Pro Ser Arg Phe Gln Lys Leu
 20 25 30
 Gly Gly Lys Glu Pro Lys Gly Val Leu Met Val Gly Pro Pro Gly Thr
 35 40 45
 Gly Lys Thr Leu Leu Ala Lys Ala Ile Ala Gly Glu Ala Lys Val Pro
 50 55 60
 Phe Phe Thr Ile Ser Gly Ser Asp Phe Val Glu Met Phe Val Gly Val
 65 70 75 80
 Gly Ala Ser Arg Val Arg Asp Met Phe Glu Gln Ala Lys Lys Ala Ala
 85 90 95
 Pro Cys Ile Ile Phe Ile Asp Glu Ile Asp Ala Val Gly Arg Gln Arg
 100 105 110
 Gly Ala Gly Leu Gly Gly Gly His Asp Glu Arg Glu Gln Thr Leu Asn
 115 120 125
 Gln Met Leu Val Glu Met Asp Gly Phe Glu Gly Asn Glu Gly Ile Ile
 130 135 140
 Val Ile Ala Ala Thr Asn Arg Pro Asp Val Leu Asp Pro Ala Leu Leu
 145 150 155 160

Arg Pro Gly Arg Phe Asp Arg Gln Val Val Val Gly Leu Pro Asp Val
165 170 175

Arg Gly Arg Glu Gln Ile Leu Lys Val His Met Arg Arg Val Pro Leu
180 185 190

Ala Pro Asp Ile Asp Ala Ala Ile Ile Ala Arg Gly Thr Pro Gly Phe
195 200 205

Ser Gly Ala Asp Leu Ala
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<210> 8

<211> 221

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> AAA ATPase superfamily PAS1 AAA domain

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1 5 10 15

Leu Glu Thr Leu Glu Trp Pro Thr Lys Tyr Glu Pro Ile Phe Val Asn
20 25 30

Cys Pro Leu Arg Leu Arg Ser Gly Ile Leu Leu Tyr Gly Tyr Pro Gly
35 40 45

Cys Gly Lys Thr Leu Leu Ala Ser Ala Val Ala Gln Gln Cys Gly Leu
50 55 60

Asn Phe Ile Ser Val Lys Gly Pro Glu Ile Leu Asn Lys Phe Ile Gly
65 70 75 80

Ala Ser Glu Gln Asn Ile Arg Glu Leu Phe Glu Arg Ala Gln Ser Val
85 90 95

Lys Pro Cys Ile Leu Phe Phe Asp Glu Phe Asp Ser Ile Ala Pro Lys
100 105 110

Arg Gly His Asp Ser Thr Gly Val Thr Asp Arg Val Val Asn Gln Leu
115 120 125

Leu Thr Gln Met Asp Gly Ala Glu Gly Leu Asp Gly Val Tyr Ile Leu
130 135 140

Ala Ala Thr Ser Arg Pro Asp Leu Ile Asp Ser Ala Leu Leu Arg Pro
145 150 155 160

Gly Arg Leu Asp Lys Ser Val Ile Cys Asn Ile Pro Thr Glu Ser Glu
165 170 175
Arg Leu Asp Ile Leu Gln Ala Ile Val Asn Ser Lys Asp Lys Asp Thr
180 185 190
Gly Gln Lys Lys Phe Ala Leu Glu Lys Asn Ala Asp Leu Lys Leu Ile
195 200 205
Ala Glu Lys Thr Ala Gly Phe Ser Gly Ala Asp Leu Gln
210 215 220

<210> 9

<211> 227

<212> PRT

<213> Cricetulus longicaudatus

<220>

<221> misc_feature

<223> AAA ATPase superfamily N-ethylmaleimide sensitive fusion protein
(NSF) AAA domain

<400> 9

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Arg Arg Ala Phe Ala Ser Arg Val Phe Pro Pro Glu Ile Val Glu Gln
20 25 30
Met Gly Cys Lys His Val Lys Gly Ile Leu Leu Tyr Gly Pro Pro Gly
35 40 45
Cys Gly Lys Thr Leu Leu Ala Arg Gln Ile Gly Lys Met Leu Asn Ala
50 55 60
Arg Glu Pro Lys Val Val Asn Gly Pro Glu Ile Leu Asn Lys Tyr Val
65 70 75 80
Gly Glu Ser Glu Ala Asn Ile Arg Lys Leu Phe Ala Asp Ala Glu Glu
85 90 95
Glu Gln Arg Arg Leu Gly Ala Asn Ser Gly Leu His Ile Ile Ile Phe
100 105 110
Asp Glu Ile Asp Ala Ile Cys Lys Gln Arg Gly Ser Met Ala Gly Ser
115 120 125
Thr Gly Val His Asp Thr Val Val Asn Gln Leu Leu Ser Lys Ile Asp
130 135 140
Gly Val Glu Gln Leu Asn Asn Ile Leu Val Ile Gly Met Thr Asn Arg
145 150 155 160

Pro Asp Leu Ile Asp Glu Ala Leu Leu Arg Pro Gly Arg Leu Glu Val
165 170 175
Lys Met Glu Ile Gly Leu Pro Asp Glu Lys Gly Arg Leu Gln Ile Leu
180 185 190
His Ile His Thr Ala Arg Met Arg Gly His Gln Leu Leu Ser Ala Asp
195 200 205
Val Asp Ile Lys Glu Leu Ala Val Glu Thr Lys Asn Phe Ser Gly Ala
210 215 220

Glu Leu Glu
225

<210> 10

<211> 253

<212> PRT

<213> Strongylocentrotus purpuratus

<220>

<221> misc_feature

<223> katanin p80 subunit WD40 repeat region

<400> 10

Lys Arg Ala Trp Lys Leu Gln Glu Leu Val Ala His Ser Ser Asn Val
1 5 10 15
Asn Cys Leu Ala Leu Gly Pro Met Ser Gly Arg Val Met Val Thr Gly
20 25 30
Gly Glu Asp Lys Lys Val Asn Leu Trp Ala Val Gly Lys Gln Asn Cys
35 40 45
Ile Ile Ser Leu Ser Gly His Thr Ser Pro Val Asp Ser Val Lys Phe
50 55 60
Asn Ser Ser Glu Glu Leu Val Val Ala Gly Ser Gln Ser Gly Thr Met
65 70 75 80
Lys Ile Tyr Asp Leu Glu Pro Ala Lys Ile Val Arg Thr Leu Thr Gly
85 90 95
His Arg Asn Ser Ile Arg Cys Met Asp Phe His Pro Phe Gly Glu Phe
100 105 110
Val Ala Ser Gly Ser Thr Asp Thr Asn Val Lys Leu Trp Asp Val Arg
115 120 125
Arg Lys Gly Cys Ile Tyr Thr Tyr Lys Gly His Ser Asp Gln Val Asn
130 135 140
Met Ile Lys Phe Ser Pro Asp Gly Lys Trp Leu Val Thr Ala Ser Glu
145 150 155 160

Asp Thr Thr Ile Lys Glu Trp Asp Leu Thr Met Gly Lys Leu Phe Gln
 165 170 175
 Glu Phe Lys Asn His Thr Gly Gly Val Thr Gly Ile Glu Phe His Pro
 180 185 190
 Asn Glu Phe Leu Leu Ala Ser Gly Ser Ser Asp Arg Thr Val Gln Phe
 195 200 205
 Trp Asp Leu Glu Thr Phe Gln Leu Val Ser Ser Thr Ser Pro Gly Ala
 210 215 220
 Ser Ala Val Arg Ser Ile Ser Phe His Pro Asp Gly Ser Tyr Leu Phe
 225 230 235 240
 Cys Ser Ser Gln Asp Met Leu His Ala Phe Gly Trp Glu
 245 250

<210> 11

<211> 253

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> putative human ortholog of katanin p80 (Hs p80) WD40 repeat region

<400> 11

Lys Thr Ala Trp Lys Leu Gln Glu Ile Val Ala His Ala Ser Asn Val
 1 5 10 15
 Ser Ser Leu Val Leu Gly Lys Ala Ser Gly Arg Leu Leu Ala Thr Gly
 20 25 30
 Gly Asp Asp Cys Arg Val Asn Leu Trp Ser Ile Asn Lys Pro Asn Cys
 35 40 45
 Ile Met Ser Leu Thr Gly His Thr Ser Pro Val Glu Ser Val Arg Leu
 50 55 60
 Asn Thr Pro Glu Glu Leu Ile Val Ala Gly Ser Gln Ser Gly Ser Ile
 65 70 75 80
 Arg Val Trp Asp Leu Glu Ala Ala Lys Ile Leu Arg Thr Leu Met Gly
 85 90 95
 Leu Lys Ala Asn Ile Cys Ser Leu Asp Phe His Pro Tyr Gly Glu Phe
 100 105 110
 Val Ala Ser Gly Ser Gln Asp Thr Asn Ile Lys Leu Trp Asp Ile Arg
 115 120 125
 Arg Lys Gly Cys Val Phe Arg Tyr Arg Gly His Ser Gln Ala Val Arg
 130 135 140

Cys Leu Arg Phe Ser Pro Asp Gly Lys Trp Leu Ala Ser Ala Ala Asp
 145 150 155 160
 Asp His Thr Val Glu Leu Trp Asp Leu Thr Ala Gly Lys Met Met Ser
 165 170 175
 Glu Phe Pro Gly His Thr Gly Pro Val Asn Val Val Glu Phe His Pro
 180 185 190
 Asn Glu Tyr Leu Leu Ala Ser Gly Ser Ser Asp Gly Thr Ile Arg Phe
 195 200 205
 Trp Asp Leu Glu Lys Phe Gln Val Val Ser Arg Ile Glu Gly Glu Pro
 210 215 220
 Gly Pro Val Arg Ser Val Leu Phe Asn Pro Asp Gly Cys Cys Leu Tyr
 225 230 235 240
 Ser Gly Cys Gln Asp Ser Leu Arg Val Tyr Gly Trp Glu
 245 250

<210> 12

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> TFIID WD40 repeat region

<400> 12

Lys Thr Ala Ser Glu Leu Lys Ile Leu Tyr Gly His Ser Gly Pro Val
 1 5 10 15
 Tyr Gly Ala Ser Phe Ser Pro Asp Arg Asn Tyr Leu Leu Ser Ser Ser
 20 25 30
 Glu Asp Gly Thr Val Arg Leu Trp Ser Leu Gln Thr Phe Thr Cys Leu
 35 40 45
 Val Gly Tyr Lys Gly His Asn Tyr Pro Val Trp Asp Thr Gln Phe Ser
 50 55 60
 Pro Tyr Gly Tyr Tyr Phe Val Ser Gly Gly His Asp Arg Val Ala Arg
 65 70 75 80
 Leu Trp Ala Thr Asp His Tyr Gln Pro Leu Arg Ile Phe Ala Gly His
 85 90 95
 Leu Ala Asp Val Asn Cys Thr Arg Phe His Pro Asn Ser Asn Tyr Val
 100 105 110
 Ala Thr Gly Ser Ala Asp Arg Thr Val Arg Leu Trp Asp Val Leu Asn
 115 120 125

Gly Asn Cys Val Arg Ile Phe Thr Gly His Lys Gly Pro Ile His Ser
 130 135 140
 Leu Thr Phe Ser Pro Asn Gly Arg Phe Leu Ala Thr Gly Ala Thr Asp
 145 150 155 160
 Gly Arg Val Leu Leu Trp Asp Ile Gly His Gly Leu Met Val Gly Glu
 165 170 175
 Leu Lys Gly His Thr Asp Thr Val Cys Ser Leu Arg Phe Ser Arg Asp
 180 185 190
 Gly Glu Ile Leu Ala Ser Gly Ser Met Asp Asn Thr Val Arg Leu Trp
 195 200 205
 Asp Ala Ile Lys Ala Phe Glu Asp Leu Glu Thr Asp Asp Phe Thr Thr
 210 215 220
 Ala Thr Gly His Ile Asn Leu Pro Glu Asn Ser Gln Glu Leu Leu Leu
 225 230 235 240
 Gly Thr Tyr Met Thr Lys Ser Thr Pro Val
 245 250

<210> 13

<211> 251

<212> PRT

<213> Thermomonospora curvata

<220>

<221> misc_feature

<223> putative serine/threonine kinase PkwA WD40 repeat region

<400> 13

Ala Ser Gly Asp Glu Leu His Thr Leu Glu Gly His Thr Asp Trp Val
 1 5 10 15
 Arg Ala Val Ala Phe Ser Pro Asp Gly Ala Leu Leu Ala Ser Gly Ser
 20 25 30
 Asp Asp Ala Thr Val Arg Leu Trp Asp Val Ala Ala Ala Glu Glu Arg
 35 40 45
 Ala Val Phe Glu Gly His Thr His Tyr Val Leu Asp Ile Ala Phe Ser
 50 55 60
 Pro Asp Gly Ser Met Val Ala Ser Gly Ser Arg Asp Gly Thr Ala Arg
 65 70 75 80
 Leu Trp Asn Val Ala Thr Gly Thr Glu His Ala Val Leu Lys Gly His
 85 90 95
 Thr Asp Tyr Val Tyr Ala Val Ala Phe Ser Pro Asp Gly Ser Met Val
 100 105 110

Ala Ser Gly Ser Arg Asp Gly Thr Ile Arg Leu Trp Asp Val Ala Thr
 115 120 125
 Gly Lys Glu Arg Asp Val Leu Gln Ala Pro Ala Glu Asn Val Val Ser
 130 135 140
 Leu Ala Phe Ser Pro Asp Gly Ser Met Leu Val His Gly Ser Asp Ser
 145 150 155 160
 Thr Val His Leu Trp Asp Val Ala Ser Gly Glu Ala Leu His Thr Phe
 165 170 175
 Glu Gly His Thr Asp Trp Val Arg Ala Val Ala Phe Ser Pro Asp Gly
 180 185 190
 Ala Leu Leu Ala Ser Gly Ser Asp Asp Arg Thr Ile Arg Leu Trp Asp
 195 200 205
 Val Ala Ala Gln Glu Glu His Thr Thr Leu Glu Gly His Thr Glu Pro
 210 215 220
 Val His Ser Val Ala Phe His Pro Glu Gly Thr Thr Leu Ala Ser Ala
 225 230 235 240
 Ser Glu Asp Gly Thr Ile Arg Ile Trp Pro Ile
 245 250

<210> 14

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> (His)6 or 6xHis tag

<400> 14

His His His His His His
1 5

<210> 15

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> katanin p80 peptide

<400> 15

Asp Ala Ser Met Met Ala Met
1 5

<210> 16

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> katanin p80 peptide

<400> 16

Ile Gln Gly Leu Arg
1 5